

Signal
peptide

AS
homology
region

1	atggatgtggggcgcgctgctgctgctctttttagctctctggcttctgtaccogtg	60
1	[M D V A A A A L P A F V A L W L L Y P W	20
61	cctctcctggggctggcccttggCgaattctcagcaggtggctgtacttttgatgatggg	120
21	P L L G S] A L G Q F S A [G G C T F D D G	40
121	ccaggggctgttgactaccaccaggatttatatcagatgacttttagtgggtccatgtcagt	180
41	P G A C D Y H Q D L Y D D F E W V H V S	60
181	gcgaggaaacctcattacctgccccCGaaatgctcgaaggttcctatatgtgttgGac	240
61	A Q E P H Y L P P E M P Q G S Y M V V D	80
241	tctcgaatcatgatcctggagaaaaagccagacttcagctgctaccatgaaggagaat	300
81	S S N H D P G E K A R L Q L P T M K E N	100
301	gacacccactgcattgattcagttacotgttatatagccagaaggggttgaaccctggc	360
101	D T H C I D F S Y L L Y S Q K G L N P G	120
361	actttgaatatcctagtttaggggtgaataaaggacctcttgctaatccaatttggaaatga	420
121	T L N I L V R V N K G E L A N P I W N V	140
421	actggattcactggtcggtgattggtcctgggctgaactagctgtgagcaccttttgccc	480
141	T G F T G R D W L R A E L A V S T F W P	160
481	aatgaataccaggtaatatattgaagctgaagctctcaggagggagaagtggttatattgcc	540
161	N E Y Q V I F E A E V S G G R S G Y I A	180
541	attgatgacatccaagtcctgagttatcctttgcgataaatctcctcattttctccgcctt	600
181	I D D I Q V L S Y] P C D K S P H F L R L	200
601	ggtgatgtggagggtcaatgctgggcagaatGctacatttcagtgctgattctcagggaga	660
201	G D V E V N A G Q N A T F Q C I A T C G R	220
661	gatGctTGcataacagttatggctgcagagacgcaatggagaagacatacccgtagcc	720
221	D A V H N K L W L Q R R N G E D I P V A	240
721	cagactaagaacataaatcagagaagatttgctgcctctttcagattgcaagaagtga	780
241	Q T K N I N H R R F A A S F R L Q E V T	260
781	aaaactgaccaggatttgaccgctgcgttaactcagtcagacgaggttctgggggtttcc	840
261	K T D Q D L Y R C V T Q S E R G S G V S	280

FIG. 1(1)

841 aattttgctcaactcattgtgagagaaccacctagaccattgctcctcccagctgctt 900
281 N F A Q L I V R E P P R P I A P P Q L L 300

901 ggtgttggcctacttacttctgtgatccaactaaatgccaactctattattggcgatggc 960
301 G V G P T Y L L I Q L N A N S I I G D G 320

961 cccatcatcctgaaagaagtagatcgatgaatgacatcaggatcttggacagaaacccat 1020
321 P I I L K E V E Y R M T S G S W T E T H 340

1021 gcagtcacgcaccaacatataagttgtggcatttagaccagatacagaatacagagatc 1080
341 A V N A P T Y K L W H L D P D T E Y E I 360

1081 cgcgtcctgcttaccagacctggcgagggggaactgggctgcccaggaccaccactgac 1140
361 R V L L T R P G E G G T G L P G P P L I 380

1141 actagacggaagtgtgcagaaacctatgaggacacaaagactttaagattgctgaaatc 1200
381 T R T K C A E P M R T P K T L K I A E I 400

1201 caggcaaggcgcatgtgcagtgagtgaggactccttgggctacaacatcactcgttgcac 1260
401 Q A R R I A V D W E S L G X N I T R C H 420

1261 acctcaactgcactatctgctaccattacttccgtggccacaatgagagcagggcgagac 1320
421 T F N V T I C Y H Y F R G H N E S R A D 440

1321 tgcttggacatggacccccaaagccccctcagcatgttgtgaaccatctgccacctacac 1380
441 C L D M D P K A P Q H V V N H L P P Y T 460

1381 aatgtcagcctcaagatgatcctaaccaaccagagggaaggagagcggaagagaca 1440
461 N V S L K M I L T N P E G R K E S E E T 480

1441 atcatccaaactgatgaagatgtgcccggtgctgcccagtcacatccctccaaaggaaac 1500
481 I I Q T D E D V P G P V P V K S L Q G T 500

1501 tcctttgaaaacagatcttccctgaactggaagagccactggaaaccgaatggaattatc 1560
501 S F E N K I F L N W K E P L E P N G I I 520

1561 actcagtatgaggtgagctatagcagcataagatcatttgaccctgctgttccagtggt 1620
521 T Q Y E V S Y S S I R S F D P A V P V A 540

1621 gggccccacagactgtatcaaatattatggaatagtacacaccatgtatttatgcatctt 1680
541 G P P Q T V S N L W N S T H H V F M H L 560

1681 caccctggaaccacactaccagttttttataagaccagCactgtcaaaggcttttgacca 1740
561 H P G T T Y Q F F I R A S T V K G F G P 580

FIG. 1(2)

1741	gcaacagccatctctgtgaccaccaaataatctcagctccaagcttacctgacatctaagaagga	1800
581	A T A I N V T T N I S A P S L P D Y E G	600
1801	gttgatgctctctgaatgaactgccaccatcacagtactattgaggcgctgcacaa	1860
601	V D A S L N E T A T T I T V L L R P A Q	620
1861	gccaaaggctgctctatcagtgcttatcaaatgtgtgagcagcgtacaccccatcga	1920
621	A C G G A P I S A Y Q I V V E Q L H F H R	640
1921	ackagcgtgaagcggggccatgggaatgctaccaggtaccgggttacataccagaacgcc	1980
641	T K R E A G A H E C Y Q V P V T Y Q N A	660
1981	ctsaagtggggGcgcgCctattactttgcgcgagaactccccctgggaactctcccgag	2040
661	L S G G A P Y Y F A A E L P P G N L P E	680
2041	cctgctcccttccagctgggtgacaacgggacctataaaggcttttggaacctccccctg	2100
681	P A P F T V G D N R T Y K G F W N P P L	700
2101	gccccccgcaaggatcacacatctattttccaagogatgagcagtggtgggaaggaaact	2160
701	A P R K G Y N I Y F Q A M S S V E K E T	720
2161	aaaaccocatgtgtgaogaattgtctacaaaagcagcagcaacAagaagaaccagaagtgtac	2220
721	K T Q C V R I A T K A A A T E E P E V I	740
2221	ccagacccggcaaaGCagacagacagagtggtgaaattcgggGCatcagtgctgtgcac	2280
741	P D P A K Q C T D R V V K I A G I S A G I	760
2281	ctagtgctcatctctctcctgctggtgtgcatagttaattgtgaaaagagcaagctgtgt	2340
761	L V F I L L L L V I V I V I K K S K L A	780
2341	aagaagcgcaaaagatgcaatggggaacacacgtcaggagatgacccacatggtgaatgct	2400
781	K K R R K D A M G N T R Q E M T H M V N A	800
2401	atggaccgaagtattgctgacgacagaccctcgatgcagaagaccccccttccctcacc	2460
801	M D R S Y A D Q S T L H A E D P L S L T	820
2461	ttcaTggaccaacataactctcagtccaagattgccaatgatccactgtgcgcagtgcc	2520
821	F M D Q H N F S P R L P N D P L V P T A	840
2521	gtgttagatgagaaccacagtgccacacagcagctctagtgtctCctgtagtctcctga	2580
841	V L D E N H S A T A E S S R L L D V P R	860

FIG. 1(3)

PTase
Domain I

2581	tacctctgcgaaggacagagtcaccttatcagacaggacagctgcaccagccatcagg	2640
861	Y L C E G T E S P Y Q T G Q L H P A I R	880
2641	gtggccgacttactgcagcacattaacctcatgaagacatcagacagctatgggttcaaa	2700
881	V A D L L Q H I N L M K T S D S Y G F K	900
2701	gaggaatcagagagCttctttgaaggccagtcagcctcttgggatgtggctaaaaaggat	2760
901	E E Y E S F F E G Q S A S W D V A K K D	920
2761	caaaacagagcaaaagaccgatacgggaacattatcgcatatgatcactccagagtcac	2820
921	Q N R A K [N R Y G N I I A Y D H S R V I	940
2821	ctgcaacctgtggaagatgacccttcttcagattacataatgccaaactacatcgacatt	2880
941	L Q P V E D D P S S D Y I N A N Y I D I	960
2881	tggtgtgtacagggtatggctaccagagaccaagccactacattGCaactcaaggccaggt	2940
961	W L Y R D G Y Q R P S H Y I A T Q G P V	980
2941	catyaaaccgtatatgatttttGGAggatggtgtggcagagcagctctgcctgtattgtg	3000
981	H E T V Y D F W R M V W Q E Q S A C I V	1000
3001	atggtcactaaTttagtGgaagtTGGCCGggtgaaatgctataaatattggcctgatgat	3060
1001	M V T N L V E V G R V K C Y K Y W P D D	1020
3061	actgaggtttatggtgacttcaagtcacCTGctagaatggagccacttctgtagtat	3120
1021	T E V Y G D F K V T C V E M E P L A E Y	1040
3121	gtcgttaggcattccaccttggaaaggagggtctataatgaaatccgtgaagtcaaacag	3180
1041	V V R T F T L E R R G Y N E I R E V K Q	1060
3181	ttccacttcactggctggcctgacctggtgttccataccacgcaacagggtcctctgtca	3240
1061	F H F T G W P D H G V P Y H A T G L L S	1080
3241	tttatccggagagtcgaagctatctaaccctcccagtgctgggcccattgtgtacactgc	3300
1081	F I R R V K L S N P P S A G P I V V H C	1100
3301	agtgtgctgtctggggccacaggctgttacattgttattgacataatgtggacatggct	3360
1101	S A G A G R T G C Y I V I D I M L D M A	1120
3361	gaaagagaggtgtgtgttgacatctacaactgtgtgaaagccttacgatctcggcgcat	3420
1121	E R E G V V D I Y N C V K A L R S R R I	1140
3421	aatatggtacagacagaggaacagtcacattttttatcatgatgccattttagaagcctgc	3480
1141	N M V Q T E E Q Y I F I H D A I L E A C	1160

FIG. 1(4)

PTPase
Domain II

3481	ttatgtggagaaactgccatccctgtgtgtaatttaaagctgcataattttgatgatg	3540
1161	L C G E T A I P V C E F K A A Y F D M I	1180
3541	cgaatagactctcagactaactcctctcatctcaagaatgaatttcagactctgaattcg	3600
1181	R I D S Q T N S S H L K D E F Q T L N S	1200
3601	gtcaccctcgactacaagctgaagctgcagcatagcctgccaaggaacctgac	3660
1201	V T P R L Q A E D C S I A C L P R N H D	1220
3661	aagaaccgtttcatggatattgctccacctgacagatgtctgctcttttttaattacaatt	3720
1221	K N R F M D M L P P D R C L P F L I T I	1240
3721	gatggggagagCagtaactacatcaatgtctgctcttatggatagctataggcagccagca	3780
1241	D G E S S N Y I N A A L M D S Y R Q P A	1260
3781	gctttcatctgCacacaatacccaactgccaaacactgtgnaagacttCtggagattagta	3840
1261	A F I V T Q Y P L P N T V K D F W R L V	1280
3841	tatgattAgggatgtacctccatctgtgatgtcaaatgaagtggacctgtctcagggtctgc	3900
1281	Y D Y G C T S I V M L N E V D L S Q G C	1300
3901	ccacagctactggccagaagaagggaatgctgcgatattggtctctatccaagtggatgtatg	3960
1301	P Q Y W P E E G M L R Y G P I Q V E C M	1320
3961	tctgttcaatggactgtgatgtgatcaatcgaaatcttttagaatatgcaacctaacgaga	4020
1321	S C S M D C D V I N R I F R I C N L T R	1340
4021	ccacaggagggtctatctgatggtacaacagTTCagtaacctagggtgggtcttctcatoga	4080
1341	P Q E G Y L M V Q Q F Q Y L G W A S H R	1360
4081	gaagtgcctgggtccaaacgctcgtttttgaaattgatactgCaggtggaaaaatggcaa	4140
1361	E V P G S K R S F L K L I L Q V E K W Q	1380
4141	gaggaaatgtgaagaagggggaaggccggacaatcatccactgcttgaatggcggtgggCGC	4200
1381	E E C E E G E G R T I I H C L N G G G R	1400
4201	agtggcatgttctgtgcatagggcattgtgtgtggagatggtgaagcggcaaaatgtgtg	4260
1401	S G M F C A I G I V V E M V K R Q N V V	1420
4261	gatgtttttcatgcagtaaaagcgtgaggaacagcaagccaaacatggtggaagccccc	4320
1421	D V F H A V K T L R N S K P N M V E A P	1440
4321	gagcagctatcgtTttttgctatgatgtggcggttagtagtacctggagctcctcatag	4374
1441	E Q Y R F C Y D V A L E Y L E S S	1458

FIG. 1(5)

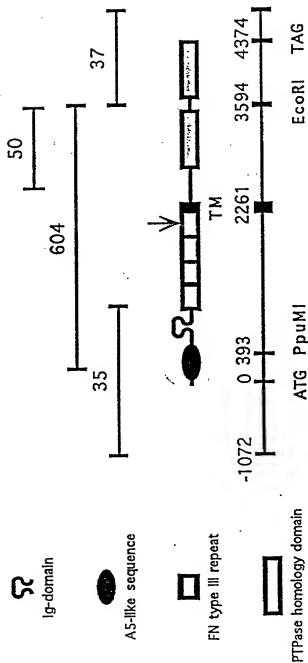


FIG. 2

[illegible]

FIG. 3

I (296) * P Q L L G V O P T V L L I Q L A N N S I I G G P I L K E V E Y R M T S G S T H T H A N N A P T Y K L W H L D P D T E . Y E I R V I L L T R P G E G T Q L P O P P L I T R T *
 II (392) P . K T L K I A B I Q A . . R R I A V D W E S L G V N T R C H T F N V T I C H Y F R G H N E S R A D C L D M D F K A . . . P O H V O N H L P P Y T N V S I R M I L . T N P E G
 III (493) P V K S L Q O T S F E . . . N K I F L N W K E L E P N G I I T Q Y E V S Y S S I R S F D P A V P A G P P O T V S N L M I S T H H V F M H L H P G T T Y Q F F I R A S T V K G F
 IV (596) P D Y E G V D A S L N E T A T T I V L L R P A Q A K G A F I S A Y Q I W E Q L H P H E T K R . E G A N E C Y O V P V T Y Q N A L S G G A P Y Y P A E L P P O N L P
 P E N - I I I (7) P P T N L H L E A N P D T . G V L T W S W E R S T T P D . . I T G Y R I T T T P T N G Q Q G S L E E V H I A D Q S S C T F D N L S P G L E Y N V S Y I . T V K D D

FIG. 4

PTP-K (34) GGCTFDDPGACDHYHQLYDDFEWVHSAQE, PHYLPEMPQGSYAVVDSNNHDPCEKARLQLPMTKEN, DTHCIDFSYLLYSQK
 PTP-H (26) GGCLFDEPYSTCGYQADEDDEFWQVNTLTPT, SDPMPSGSEMLVNTSGDE, QRAHLLLPOLKEN, DTHCIDFHYFVSSKS
 A5 (651) CRFGWSQKTCVNWQHDISSDLKWAFLNSKTGP, VQDHTGDGNFIYSEADHERHARLMSPVSSSSRAHCLTFWYHM...D
 Consensus -----C-----D--D--W--N--T-P-----G-F-----E--A--P-----HC--F--Y-----

PTP-K GLNPCTLNILVRVN, KGPLANPIWNVTGTCROWLRAELAVSTWPNEYQVIFEAVVSGRSGYTAIDDIQVLSY
 PTP-H NAAPGLLNIVVKN, KGPLNGPIWNISGDPTRTHRAELASTWPNFYQVIFEV, VTSCHOGYLAIDEVKVLGH
 A5 GSHVGTLSIKLYEMEEDPDOTLTWTSNGQDQWKEARWLHKTMQ, YQVIVEC^WVGKGSAGGIADVDDIIIANH
 Consensus G---GTL-I--K-----W-VSG--G--W--A-----YQVI-E--V--G--G-IA-DDI-----H

FIG. 5

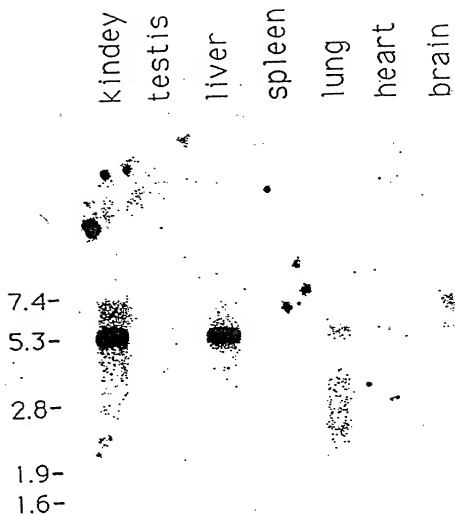


FIG. 6

Transfected:	-	-	-	+	+	+
Antibody:	pre	α - κ	α - κ	pre	α - κ	α - κ
Peptide:	-	-	+	-	-	+

211 -

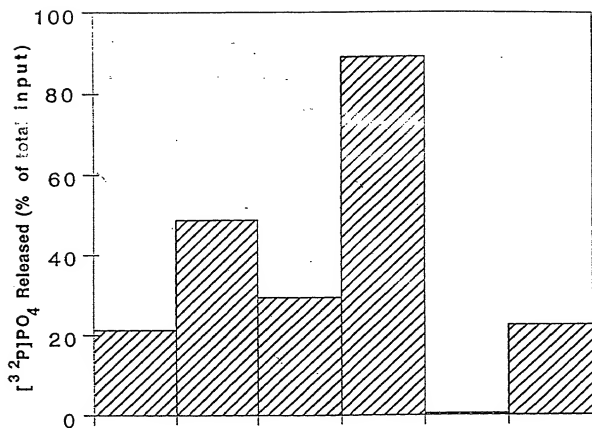
119 -

98 -

81 -

64 -

FIG. 7



Transfection	mock	κ	mock	κ	mock	κ
Antibody	pre	pre	116	116	116	116
Vanadate	-	-	-	-	+	+

FIG. 8

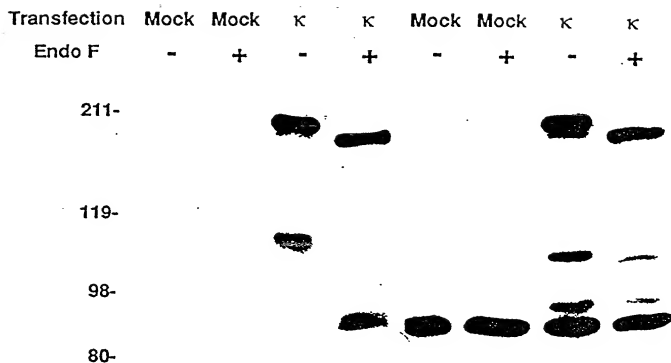


FIG. 9

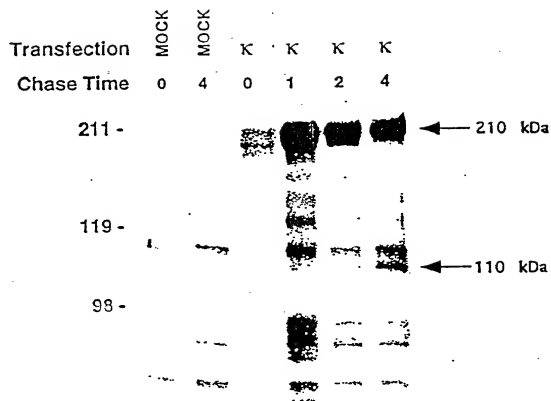


FIG. 10

09587569.100101

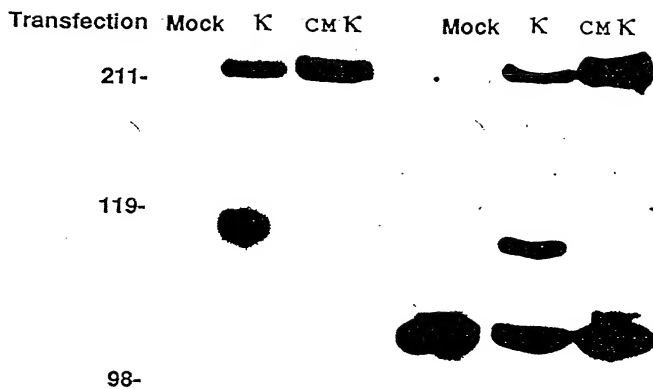


FIG. 11

Transfection Mock K K
IP 116 116 Total lysate

211-

119-



98-

FIG. 12

Figure 1 consists of two panels, A and B, showing fluorescence micrographs of Drosophila ommatidia. Panel A shows a normal ommatidium with labels SC (sensory cone), K (cone cell), I (pigment cell), L (pigment cell), and CTX (crystalline cone). Panel B shows a mutant ommatidium with labels CB (cone cell body) and DG (dendritic growth).

FIG. 13

101001-89/8860

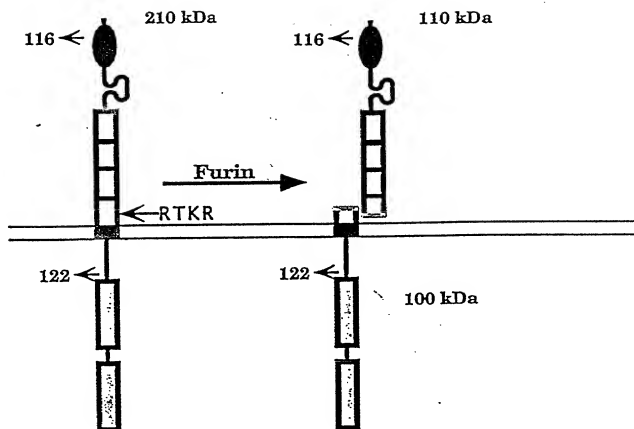


FIG. 14

921	CGAACACGAGGAGGAGCGGAGACATGGAACTGCACCAAGTTCCTGTGCATACCAAAATGCCATGAGTGGGGGTGCACC	2000
641	TT T K R E A E G A M E C Y Q V P V T Y Q N A T S G G G G A P	667
2001	GTATTACTTTCTGTCGAGAACTACCCCGCGGAAACCTACTCGAGCTGCCCGGTCTACTGTGGTGACAATTGGAAGTACC	2080
667	Y Y F A A E L F P P G N L F E P A P F T V G D N R T Y Q	693
2081	AAGGCTTTTGAACCTCCTCTTGGCTGCCCGCAAGGATACCAACTCTATTTCAGGGCGTAGGACGTGTGGAGAAAGAA	2160
694	G F W N L L F A P R K G Y N I Y F Q A M S S V E K E	720
2161	ACTAAAAACCGATGCTGATCGCAATTCGTACAAAGACAGCAACGAAGAAACGAAAGTATCCGCAATGCCCGCAAGGAGAC	2240
721	T K T Q C V C R I A A A T E E P E V I P D P A K Q T	747
2241	AGACAGAGTGTGAAATAGACGAAATATAGCTGTGAAATTTTGGTGTTATCATCTCCTCTCTGCTGATTAATTTG	2320
747	D R V V K I A G I S A G I L V F I L L L V I L I V	773
2321	TAAAAAGACCAAACTTGCTATAAAAGCGAAGAGTGCATGGGGAAATACCCGGCAGGAGATGACTACATGCTGTAATGCA	2400
774	K K S K L A K R K D A M G N T R G E M T M V N A	800
2401	ATGGATCGAAGTATGTGCTGATCGAGCACTCTGCATGCAGAAAGTCTCTTTTCCATACACCTTCATGGACCAACATAACTT	2480
801	M D T S R Y A D Q S T L L H A E D F L S I T F M Q D H N F	827
2481	TAGTCCAGATATGACCAACAGCTGTCTACAGAAAGCTCCAGCTCCCTCTAGAGTACTCTCGCTACTCTGTGAGGGGA	2560
827	S P R Y E N H S A T A E S S R L L D V P R Y I L C E G T	853
2561	CGGAATCCCYCTTACCAAGACAGCAGCTGCATCCAGCAGTACAGGGTAGCTGATTATTCAGCAGCAATAATCTCATGAAG	2640
854	E S P Y Q T G Q L H P A I R V A D L L Q H I N L M K	880
2641	ACATCAGACAGCTATGGGTTCAAAGAGGAATATGAGAGCTTTTTTGAAGGACAGTCAGCACTTCTGGGATGTAGTAAAAA	2720
881	T S D S Y G E F K E E Y E S F F E G Q S A S W D V A K K	907
2721	AGATCAAAATAGAGCAAAACAGATGAGAACTATGACATATGATCATCTCAGAGTATTTTGCACACCGTAGAGG	2800
907	D Q N R A K N R I A G Y G N I I A Y D H S R V I L Q P V E D	933
2801	ATGATCCTCTCATGATTATTAATGCCAACTATATGATGGCTACCGAGACCAAGTCAATTCATGCAACCCAAAGT	2880
934	D P S S D Y I N A N Y I D G Y Q R P S H Y I A T Q O	960
2881	CCGCTCATGAAACAGTGTATGATTCTGGAGAGTATTGTGGCAAGAACATCTGCTTGCATTGTATGGTGTACAAATTT	2960
961	F V H E T Y I W D F N R M I W Q E Q S A C T I M V T N L	987
2961	AGTTGAGGTTGGCGGGGTAAATGTCTATAATTTGGCTGATGATCTAGTAGTATTATGTGACTCAAGATTAACGTGTG	3040
987	V E V G R V K C Y K Y W P D D T E V Y Y G D F K V T C V	1013
3041	TAGAAATGGAAACCATCTGCTGAATATGTATGAGCAATCACCTTGGAAGAGGGGGTACAATGAATCCGTGAAAT	3120
1014	E M E P L A E Y V V R T F T L L E R R Y N N E I R E	1040
3121	AAACAGTTCACATCTGCGGGCTGGCGGACCATGGAGTGGCCCTACATGCTACAGGGCTGCTTTGCTTTATCCGGGGAGT	3200
1041	K Q F H F T G W F D H G V P Y H A T G L S F E I R R V	1067
3201	CAAGTTATCAAACTCTCCAGCTGTGGCGCATCGTGTGATATCGCACTTGTGCTGGGACGAACTGGCTGCTACATTTG	1280
1067	K L S N P P S A G P I V V H C S A G A G A R T G C Y I V	1093
3281	TGATTGACATCATGCTAGACATGGCTGAAGAGAGGGTGTGTTGATATTACAAATTGTGTCAAAGCCTTAAGATCTCGG	3360
1094	I D I M L D M A E R E G V D I T Y N C V K A L R S R	1120
3361	CGTATTAAATATGGTCCAGACAGAGGAACAGTACATTTTATTATCATGATGCCATTTTAGAAGCTGCTTATGTGGAGAAAC	3440
1121	R I N M V Q T E E Q Y X I F I H D A I L E A C L G E T	1147
3441	TGCCATCTCTGTGTGAAATTTAAAGCTGCATATTTTGATATAGTAAGTAGACCTCCAGCACTAATCTTCCATCTCAATCA	3520
1147	A I P V C E F K A A Y F D M I R I D S Q A G T N S S H L K	1173
3521	AGGATGAATTTAGACATCTGAAATTCAGTACCCCTGCACTACAGCTGAAGACGCACTATAGGCTGCTCGCAAGGAAC	3600
1174	D E F Q T L N S V T E R F L Q A E D C S I A C L P R N	1200
3601	CATGACAAGAACCCTTTTCATGAGCATGCTGCCACTGCAGACATGTCTGCGCTTTTAAATACAAATTGATGGGGAGAGCAG	3680
1201	H P K N R N R F M D M L P P D R C L F F L I T I D G J E S S	1227
3681	TAACTACATCAATGCTGCTCTTATGGACAGCTACAGGCAACCAAGCTGCTTCATCGTATACAAATCCCTTCGCCAAACA	3760
1227	N Y I N A I L M D S Y R Q F A A P I T Q Y P L F N T	1253
3761	CTGTAAAGACTCTGAGGATATGTTATGATATATGCTCCATCTGCTATGTGAATGAAAGCAATGCACTTCTGCCAC	3840
1254	V K D F W L R L L V Y D Y G C T S I Y V M L N E V D L S Q	1280

09867569 101111

3841	GGCTGCCCCAGTACTGGCCAGAGGAAGGGATGCTACGATATGGCCCCATCCAAAGTGAATGTATGTTGTTCAATGGA	3920
1281	G C F Q Y W F E E G M L R Y G P I Q V E C M S C S M D	1307
3921	CTGTGATGTGATCAACCGGATTTTAGGATATGCAATCTAACAGACCCAGGAAGGTTATCTGATGGTGCAACAGTTTC	4000
1307	C D V I N R I F R I C H L T R F Q E G Y L M V Q Q F Q	1333
4001	AGTACCTAGGATGGGCTTCTCATCGAGAAGTGCCCTGGATCCAAAAGGTCATTCTTGAAACTGATACTTCAGGTGGAAGG	4080
1334	Y L G W A S H R E V P G S K R S F L K L I L Q V E K	1360
4081	TGGCAGGAGGAATCCGAGGAAGGGGAGGCCGACGATTATCCACTGCCTAAATGGTGGCGGGCGAAGTGGCATGTTCTG	4160
1361	W Q E E C E E G E G R T I I E C L N G G G R S G M F C	1387
4161	TGCTATAGGCAATGTTGTTGAAATGGTGAACGGCAAAATGTTGTGATGTTTTCCATGCAGTAAGACACTGAGGAACA	4240
1387	A I G I V V E M V K R Q N V V D V F H A V K T L R N S	1413
4241	GCAAGCCAAACATGGTGGAAAGCCCCGGAGCAATACCGTTTCTGCTATGATGTAGCTTTGGAGTACCTGGAAATCATCTTAG	4320
1414	X P N M V E A P E Q Y R F C Y D V A L E Y L E S S	1439
4321	TTGGGTGAGACTCTTTAAAGTGCAATCCATGAAGAAACCTGTCCATCTATTGAGCCAGCAGCTGTTGTACCTGTTACACTT	4400
4401	GTGCAGAAAGATTTAAATGTGGGGGGTGGGAGACTTTTACATTTGAGAGGTAAGATTTTTTTTATGAAGTTGATAT	4480
4481	CTTATATTAAGCACTGATTAATTTTTTATCTATATTAAGCAATCAACATTTTCATGCCACATAAAATTAATTAATA	4560
4561	AGAACCAGATTGAAATGAGAACGATTGGTGTGTTGTACAGTGAAATGCACCTTTTCCATGGTTTCAGGTAGTCAGC	4640
4641	TACCACATGTT 4651	

(SER IO NO: 4)

(SER IO NO: 2)

FIG. 15(3)

[illegible]

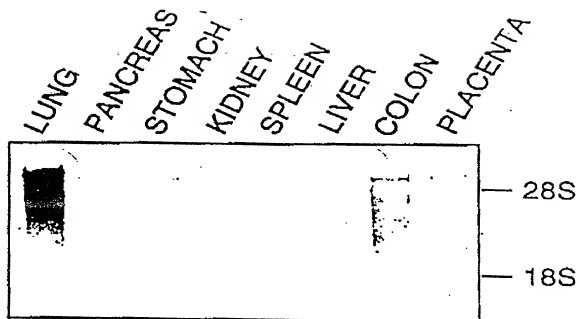


FIG. 17

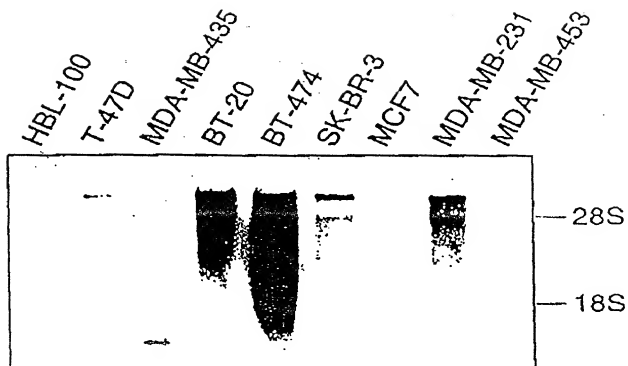


FIG. 18

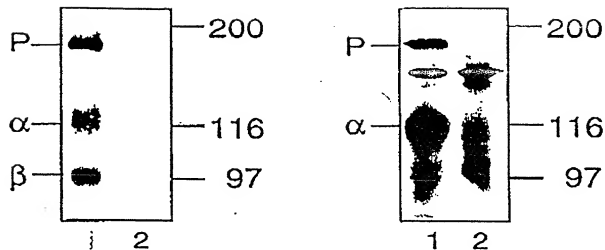


FIG. 19

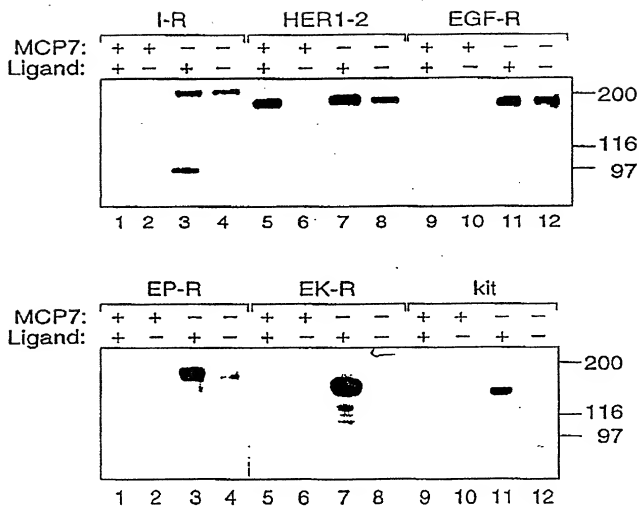


FIG. 20

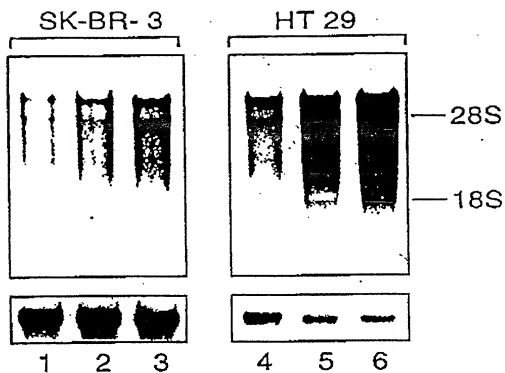


FIG. 21

1 2 3 4 5

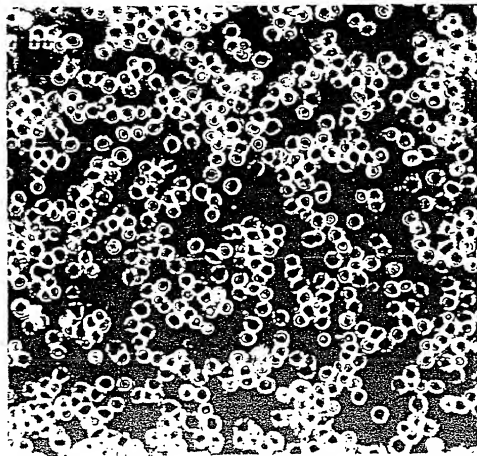
190 —
125 —
88 —
65 —
56 —



FIG. 22 A

KOTOCOT' 699/8860

Control



R-PTP-κ

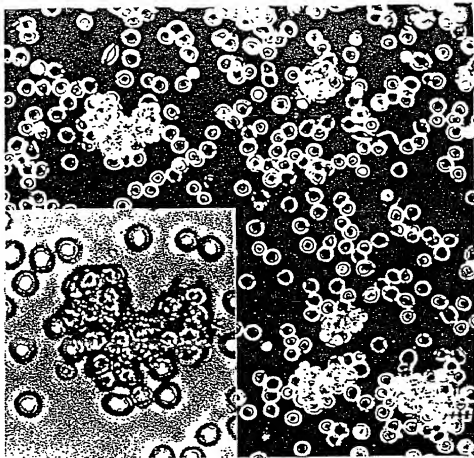


FIG. 22B

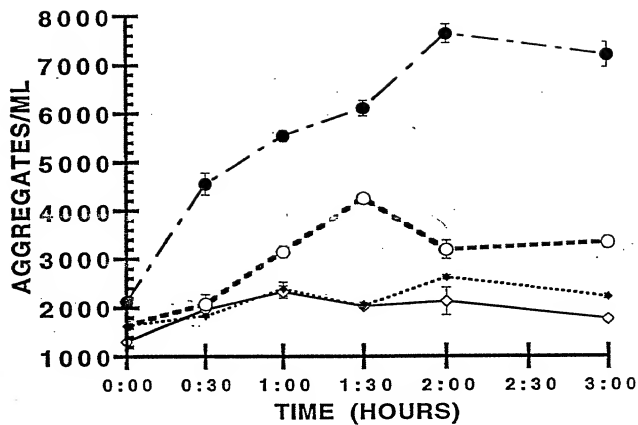


FIG. 22 C

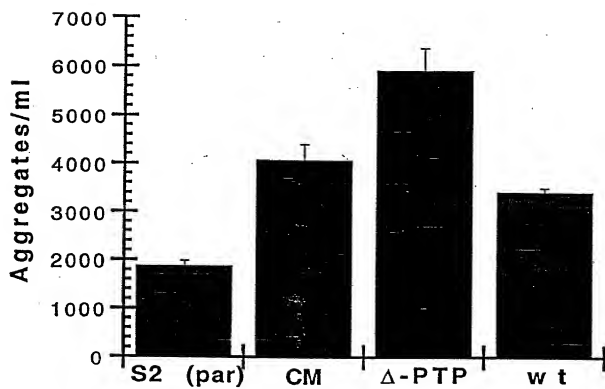


FIG. 22D

$K^-(diI) + K^+$



$K^- + K^+(diI)$



$K^+ + K^+(diI)$



FIG. 23

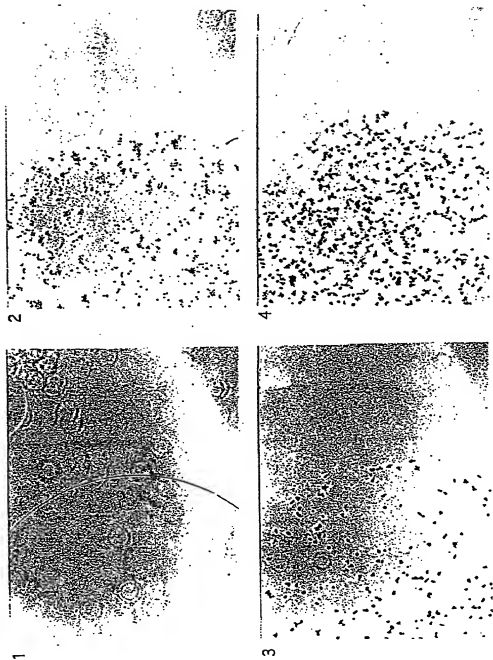


FIG. 24